

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/556,904  
Source: PLT/10  
Date Processed by STIC: 11/25/05

***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 11/25/2005

PATENT APPLICATION: US/10/556,904

TIME: 12:04:16

Input Set : A:\PA038WO\_SEQ\_listing.ST25.txt

Output Set: N:\CRF4\11252005\J556904.raw

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3 <110> APPLICANT: Cytos Biotechnology AG
4     Bachmann, Martin F
5     Gatto, Dominige
7 <120> TITLE OF INVENTION: SELECTION OF B CELLS WITH SPECIFICITY OF INTEREST: METHOD OF
8     PREPARATION AND USE
10 <130> FILE REFERENCE: C62780PC
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/556,904
C--> 12 <141> CURRENT FILING DATE: 2005-11-15
12 <150> PRIOR APPLICATION NUMBER: US 60/470,443
13 <151> PRIOR FILING DATE: 2003-05-15
15 <160> NUMBER OF SEQ ID NOS: 85
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 132
21 <212> TYPE: PRT
22 <213> ORGANISM: Bacteriophage Q beta
24 <400> SEQUENCE: 1
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27 1           5           10           15
30 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
31           20           25           30
34 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
35           35           40           45
38 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
39           50           55           60
42 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
43 65           70           75           80
46 Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
47           85           90           95
50 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
51           100          105          110
54 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
55           115          120          125
58 Asn Pro Ala Tyr
59           130
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 329
64 <212> TYPE: PRT
65 <213> ORGANISM: Bacteriophage Q beta
67 <400> SEQUENCE: 2
69 Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
70 1           5           10           15
73 Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly

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74          20          25          30
77 Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
78          35          40          45
81 Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
82          50          55          60
85 Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
86 65          70          75          80
89 Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
90          85          90          95
93 Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
94          100          105          110
97 Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
98          115          120          125
101 Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Gly Ser Gly
102          130          135          140
105 Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro
106 145          150          155          160
109 Gly Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu
110          165          170          175
113 Val Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala
114          180          185          190
117 Val Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu
118          195          200          205
121 Gly Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr
122          210          215          220
125 Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr
126 225          230          235          240
129 Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu
130          245          250          255
133 Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu
134          260          265          270
137 Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
138          275          280          285
141 Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
142          290          295          300
145 Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
146 305          310          315          320
149 Gln Ala Val Ile Val Val Pro Arg Ala
150          325
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 130
155 <212> TYPE: PRT
156 <213> ORGANISM: Bacteriophage fr
158 <400> SEQUENCE: 3
160 Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
161 1          5          10          15
164 Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
165          20          25          30
168 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

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169          35          40          45
172 Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
173          50          55          60
176 Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
177 65          70          75          80
180 Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
181          85          90          95
184 Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
185          100          105          110
188 Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
189          115          120          125
192 Ile Tyr
193          130
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 130
198 <212> TYPE: PRT
199 <213> ORGANISM: Bacteriophage GA
201 <400> SEQUENCE: 4
203 Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
204 1          5          10          15
207 Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
208          20          25          30
211 Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
212          35          40          45
215 Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
216          50          55          60
219 Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
220 65          70          75          80
223 Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
224          85          90          95
227 Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
228          100          105          110
231 Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
232          115          120          125
235 Tyr Ala
236          130
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 128
241 <212> TYPE: PRT
242 <213> ORGANISM: Bacteriophage PP7
244 <400> SEQUENCE: 5
246 Met Ser Lys Thr Ile Val Leu Ser Val Gly Glu Ala Thr Arg Thr Leu
247 1          5          10          15
250 Thr Glu Ile Gln Ser Thr Ala Asp Arg Gln Ile Phe Glu Glu Lys Val
251          20          25          30
254 Gly Pro Leu Val Gly Arg Leu Arg Leu Thr Ala Ser Leu Arg Gln Asn
255          35          40          45
258 Gly Ala Lys Thr Ala Tyr Arg Val Asn Leu Lys Leu Asp Gln Ala Asp
259          50          55          60

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262 Val Val Asp Cys Ser Thr Ser Val Cys Gly Glu Leu Pro Lys Val Arg
263 65              70              75              80
266 Tyr Thr Gln Val Trp Ser His Asp Val Thr Ile Val Ala Asn Ser Thr
267              85              90              95
270 Glu Ala Ser Arg Lys Ser Leu Tyr Asp Leu Thr Lys Ser Leu Val Ala
271              100             105             110
274 Thr Ser Gln Val Glu Asp Leu Val Val Asn Leu Val Pro Leu Gly Arg
275              115             120             125
278 <210> SEQ ID NO: 6
279 <211> LENGTH: 132
280 <212> TYPE: PRT
281 <213> ORGANISM: Bacteriophage Q-beta
283 <400> SEQUENCE: 6
285 Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys
286 1              5              10              15
289 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
290              20              25              30
293 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
294              35              40              45
297 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
298              50              55              60
301 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
302 65              70              75              80
305 Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
306              85              90              95
309 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
310              100             105             110
313 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
314              115             120             125
317 Asn Pro Ala Tyr
318              130
321 <210> SEQ ID NO: 7
322 <211> LENGTH: 132
323 <212> TYPE: PRT
324 <213> ORGANISM: Bacteriophage Q-beta
326 <400> SEQUENCE: 7
328 Ala Lys Leu Glu Thr Val Thr Leu Gly Lys Ile Gly Lys Asp Gly Lys
329 1              5              10              15
332 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
333              20              25              30
336 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
337              35              40              45
340 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
341              50              55              60
344 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
345 65              70              75              80
348 Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
349              85              90              95
352 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu

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353          100          105          110
356 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
357          115          120          125
360 Asn Pro Ala Tyr
361          130
364 <210> SEQ ID NO: 8
365 <211> LENGTH: 132
366 <212> TYPE: PRT
367 <213> ORGANISM: Bacteriophage Q-beta
369 <400> SEQUENCE: 8
371 Ala Arg Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys
372 1          5          10          15
375 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
376          20          25          30
379 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
380          35          40          45
383 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
384          50          55          60
387 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
388 65          70          75          80
391 Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
392          85          90          95
395 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
396          100         105         110
399 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
400          115         120         125
403 Asn Pro Ala Tyr
404          130
407 <210> SEQ ID NO: 9
408 <211> LENGTH: 132
409 <212> TYPE: PRT
410 <213> ORGANISM: Bacteriophage Q-beta
412 <400> SEQUENCE: 9
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418 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
419          20          25          30
422 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
423          35          40          45
426 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
427          50          55          60
430 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
431 65          70          75          80
434 Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe
435          85          90          95
438 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
439          100         105         110
442 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
443          115         120         125

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Input Set : A:\PA038WO\_SEQ\_listing.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2205 M:220 C: Keyword misspelled or invalid format, &lt;213&gt; ORGANISM for SEQ ID#:80